



SEQUENCE LISTING

<110> Daniel E. Afar
Rene S. Hubert
Kahan Leong
Arthur B. Raitano
Douglas C. Saffran

<120> NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
AND THERAPY OF PROSTATE AND COLON CANCER

<130> 129.8USU1

<140> 09/323,597

<141> 1999-06-01

<150> 60/087,598

<151> 1998-06-01

<150> 60/091,474

<151> 1998-06-29

<150> 60/129,521

<151> 1999-04-14

<160> 17

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<212> DNA

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Met Ala
1

ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat 165
Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
5 10 15

gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc 213
Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
20 25 30

act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc 261
Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
35 40 45 50

RECEIVED
MAR 03 2003
TECH CENTER 1600/2900

H9

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| cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc | 309 |
| Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys | |
| 55 60 65 | |
| acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag | 357 |
| Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys | |
| 70 75 80 | |
| aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct | 405 |
| Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala | |
| 85 90 95 | |
| gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc | 453 |
| Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser | |
| 100 105 110 | |
| aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct | 501 |
| Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser | |
| 115 120 125 130 | |
| aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat | 549 |
| Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn | |
| 135 140 145 | |
| cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca | 597 |
| Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser | |
| 150 155 160 | |
| tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag | 645 |
| Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu | |
| 165 170 175 | |
| aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt | 693 |
| Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe | |
| 180 185 190 | |
| tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt atg | 741 |
| Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met | |
| 195 200 205 210 | |
| aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac | 789 |
| Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr | |
| 215 220 225 | |
| cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata | 837 |
| His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile | |
| 230 235 240 | |
| gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc | 885 |
| Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly | |
| 245 250 255 | |
| ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac | 933 |
| Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His | |
| 260 265 270 | |
| gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg | 981 |

| | |
|---|------|
| Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp | |
| 275 280 285 290 | |
| atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg | 1029 |
| Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp | |
| 295 300 305 | |
| cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat | 1077 |
| His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr | |
| 310 315 320 | |
| gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac | 1125 |
| Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp | |
| 325 330 335 | |
| tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct | 1173 |
| Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro | |
| 340 345 350 | |
| ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc | 1221 |
| Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly | |
| 355 360 365 370 | |
| atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg gcc | 1269 |
| Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala | |
| 375 380 385 | |
| acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg | 1317 |
| Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val | |
| 390 395 400 | |
| ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac aac | 1365 |
| Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn | |
| 405 410 415 | |
| ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc | 1413 |
| Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val | |
| 420 425 430 | |
| gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac | 1461 |
| Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn | |
| 435 440 445 450 | |
| aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc | 1509 |
| Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala | |
| 455 460 465 | |
| aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg gac | 1557 |
| Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp | |
| 470 475 480 | |
| tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc | 1608 |
| Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly | |
| 485 490 | |
| ttgacgtcgt tttaacaagaa aacaatgggg ctgggttttgc ttccccgtgc atgatttact | 1668 |
| cttagagatg attcagaggt cacttcattt ttatttaaaca gtgaacttgt ctggcaaaaa | 1728 |

aaaaaaaaaa

1738

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<212> PRT
<213> Homo sapiens

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35 40 45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
100 105 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
115 120 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
130 135 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
145 150 155 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
165 170 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
180 185 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
195 200 205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
210 215 220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225 230 235 240
Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
245 250 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
260 265 270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
275 280 285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
290 295 300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305 310 315 320
Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
325 330 335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
340 345 350
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
355 360 365
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
370 375 380
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala

H94
CW

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 385 | | | | | 390 | | | | | 395 | | | | 400 | |
| Lys | Val | Leu | Leu | Ile | Glu | Thr | Gln | Arg | Cys | Asn | Ser | Arg | Tyr | Val | Tyr |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Asp | Asn | Leu | Ile | Thr | Pro | Ala | Met | Ile | Cys | Ala | Gly | Phe | Leu | Gln | Gly |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Asn | Val | Asp | Ser | Cys | Gln | Gly | Asp | Ser | Gly | Gly | Pro | Leu | Val | Thr | Ser |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Lys | Asn | Asn | Ile | Trp | Trp | Leu | Ile | Gly | Asp | Thr | Ser | Trp | Gly | Ser | Gly |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Cys | Ala | Lys | Ala | Tyr | Arg | Pro | Gly | Val | Tyr | Gly | Asn | Val | Met | Val | Phe |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Thr | Asp | Trp | Ile | Tyr | Arg | Gln | Met | Arg | Ala | Asp | Gly | | | | |
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| cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc | 155 |
| ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg | 203 |
| ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc | 251 |
| tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act | 299 |
| aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga | 347 |
| gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc | 395 |
| tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc | 443 |
| tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag | 491 |
| aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac | 539 |
| tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac | 587 |
| gag aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat | 635 |
| ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt | 683 |
| atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg | 731 |
| tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt | 779 |
| tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg | 827 |
| ggc ggt gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg | 875 |
| cac gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag | 923 |
| tgg atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca | 971 |
| tgg cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc | 1019 |
| tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat | 1067 |
| gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag | 1115 |
| cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca | 1163 |
| ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg | 1211 |
| gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag | 1259 |
| gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac | 1307 |
| aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac | 1355 |
| gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aac | 1403 |
| aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt | 1451 |
| gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg | 1499 |
| gac tgg att tat cga caa atg aag gca aac ggc t aatccacatg | 1543 |
| gtcttcgtcc ttgacgtcgt tttacaagaa aacaatgggg ctggttttgc ttccccgtgc | 1603 |
| atgatttact cttagagatg attcagaggt cacttcattt ttattaaaca gtgaacttgt | 1663 |
| ctggcttttg cactctctgc catactgtgc aggctgcagt ggctcccctg cccagcctgc | 1723 |
| tctccctaac cccttgtccg caaggggtga tggccggctg gttgtgggca ctggcggtca | 1783 |
| attgtggaag gaagagggtt ggaggctgcc cccattgaga tcttcctgct gagtcctttc | 1843 |

caggggcca ttttgatga gcatggagct gtcacttctc agctgctgga tgacttgaga 1903
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 ggggccactt ggtagtgtcc ccagcctact tcacaagggg attttgctga tgggttctta 2023
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 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met

305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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 485 490

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 gcacctgcag cggctgccct ctggggccac ttggtagtgt cccagccta cctctccaca 180
 aggggatttt gctgatgggt tcttanagcc ttagcagccc tggatggtgg ccagaaataa 240
 agggaccagc ccttcatggg tggtagctg gtantcactt gtaaggggaa cagaaacatt 300
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 <223> DNA Adaptor 2

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 <223> PCR Primer 1

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 <223> Nested Primer (NP) 1

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 <223> Nested Primer (NP) 2

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agtcttcctg ctgagtcctt tcc 23

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